GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 14, 2003, 09:22:34 ; Search time 42.0962 Seconds
(without alignments)
2108.144 Million cell updates/sec

Title: US-09-836-077-3
Perfect score: 3615
Sequence: 1 MTPPPPGRAAPSAPRARVPG.....LAASLWLGVLPTLTLGLLVH 666

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

arched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3615	100.0	666	20	AAY39445	Human semaphorin Z
2	3615	100.0	666	20	AAY28552	SBSEMVL polypeptid
3	3615	100.0	666	20	AAW92804	EP-892047 Seq ID 3
4	3615	100.0	666	21	AAY82433	Human CDw108 prote
5	3615	100.0	666	21	AAY55009	Human semaphorin,
6	3615	100.0	666	22	AAE02650	Human Sema7A prote
7	3443	95.2	634	21	AAY56854	Human semaphorin K
8	3214	88.9	664	21	AAY82434	Mouse CDw108 prote
9	2079	57.5	379	22	AAB93440	Human protein sequ
10	1897	52.5	394	20	AAW92805	EP-892047 Seq ID 4
11	1345.5	37.2	606	21	AAY56855	Semaphorin K1 poly
12	1029	28.5	215	20	AAY28553	SBSEMVL polypeptid
13	680.5	18.8	893	23	ABB97964	Human protein sequ
14	674.5	18.7	832	22	AAE03818	Human gene 1 encod
15	674.5	18.7	832	23	ABG64522	Human albumin fusi
16	674.5	18.7	837	21	AAY99410	Human PRO1480 (UNQ
17	674.5	18.7	837	22	AAU29250	Human PRO polypept
18	674.5	18.7	837	22	AAB66159	Protein of the inv
19	654.5	18.1	771	16	AAR71380	Human semaphorin I
20	654.5	18.1	771	22	AAG62726	Amino acid sequenc
21	649.5	18.0	796	19	AAY21264	Human semaphorin I
22	637.5	17.6	791	23	AAU77413	Human NOV7 protein
23	617	17.1	749	22	AAG62727	Amino acid sequenc
24	601.5	16.6	861	18	AAW17658	Mouse CD100 antige
25	598.5	16.6	861	19	AAW58540	Human semaphorin.
26	598.5	16.6	861	22	AAB81035	Murine CD100 amino
27	598.5	16.6	861	22	AAB51251	Mouse CD100 protei
28	597	16.5	785	22	AAG62731	Amino acid sequenc
29	591.5	16.4	751	20	AAW30617	Human semaphorin E
30	591.5	16.4	751	21	AAB28379	Clone BR533_4. Ho
31	591.5	16.4	751	22	AAG62728	Amino acid sequenc
32	590	16.3	681	21	AAB01396	Neuron-associated
33	570	15.8	862	18	AAW17657	Human CD100 antige
34	570	15.8	862	22	AAB81036	Human CD100 amino
35	570	15.8	862	22	AAB51252	Human CD100 protei
36	566	15.7	775	19	AAW63748	Human semaphorin.
37	558	15.4	775	20	AAY43090	Mouse semaphorin H
38	548.5	15.2	777	20	AAY27127	Human brain tissue
39	548.5	15.2	777	21	AAY99427	Human PRO1491 (UNQ
40	548.5	15.2	777	22	AAU29197	Human PRO polypept
41	548.5	15.2	777	22	AAB66176	Protein of the inv
42	543	15.0	477	16	AAR74175	Human collapsin.
43	536	14.8	770	22	AAB88349	Human membrane or
44	535.5	14.8	777	20	AAY43091	Mouse semaphorin H
45	535.5	14.8	777	22	AAG62730	Amino acid sequenc

ALIGNMENTS

RESULT 1
AAY39445
ID AAY39445 standard; Protein; 666 AA.
XX
AC AAY39445;
XX
DT 01-DEC-1999 (first entry)
XX
DE Human semaphorin ZSMF-7.
XX
KW Semaphorin; transmembrane; secreted; neuroregeneration;
KW immunosuppression; diabetes; multiple sclerosis; rheumatoid arthritis;
KW proliferation; differentiation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 561..620
FT /note= "Ig-like domain"
XX
PN WO9945114-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US04758.
XX
PR 03-MAR-1998; 98US-0076611.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Holloway JL, Lofton-Day CE;
XX
DR WPI; 1999-540845/45.

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DR   N-PSDB; AAZ20985, AAZ20986.
XX
PT   New isolated human semaphorin ZSMF-7 polypeptides, used to develop
PT   products for treating e.g. immunodeficiencies, autoimmune diseases,
PT   inflammation, graft rejection and infective diseases -
XX
PS   Claim 6; Page 101-102; 124pp; English.
XX
CC   This sequence represents human ZSMF-7 semaphorin. The cDNA was
CC   isolated and amplified from a human testis cDNA library using PCR
CC   primers ZC16189 (AAZ20989) and ZC16188 (AAZ20990) which had been
CC   designed based upon an incomplete clone obtained from a human placenta
CC   library. Semaphorins have a variety of roles. They influence the
CC   direction and degree of axon and dendrite growth in nervous tissue, and
CC   may thus be useful as therapeutic agents for various neurodegenerative
CC   conditions. They are active in defining and directing development of
CC   various tissues and organs including those associated with muscle,
CC   fibroblasts, reproductive, endocrine and lymphatic tissues. ZSMF-7 plays
CC   a role as a mediator of immunosuppression, in particularly the activation
CC   and regulation of T lymphocytes. ZSMF-7 polypeptides would be useful
CC   additions to therapies for treating immunodeficiencies. ZSMF-7 is
CC   expressed in activated lymphocytes (MRL cells) and not in resting
CC   lymphocyte cells (CD4+ and CD8+) suggesting that it would be a useful
CC   tool for diagnosis and treatment of conditions where selective
CC   elimination of inappropriately activated T cells would be beneficial,
CC   such as in autoimmune diseases, in particular insulin dependent
CC   diabetes mellitus, rheumatoid arthritis and multiple sclerosis. ZSMF-7
CC   polypeptides can be used in vivo as anti-inflammatory agents,
CC   for inhibition of antigen in humoral and cellular immunity and for
CC   immunosuppression in graft and organ transplants.
XX
SQ   Sequence   666 AA;

  Query Match            100.0%;  Score 3615;  DB 20;  Length 666;
  Best Local Similarity  100.0%;  Pred. No. 5.3e-304;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MTPPPPGRAAPSAPRARVPGPPARLGLPLRLRLLLLLWAAAASAQGHLRSGPRIFAVWKG 60
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Db      1 MTPPPPGRAAPSAPRARVPGPPARLGLPLRLRLLLLLWAAAASAQGHLRSGPRIFAVWKG 60

Qy     61 HVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 HVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSC 120

Qy    121 LDKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVPLGEMRGYAPFSPDENSLV 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LDKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVPLGEMRGYAPFSPDENSLV 180

Qy    181 LFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKI 240

Qy    241 YYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKNF 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKNF 300

Qy    301 NRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFRTSSLKGYHSSLPN 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFRTSSLKGYHSSLPN 360

Qy    361 PRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQASH 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQASH 420

Qy    421 GETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVS 480
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Db    421 GETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVS 480

Qy    481 SQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSSERSVLQSINPAEPHKE 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 SQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSSERSVLQSINPAEPHKE 540

Qy    541 CPNPKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCILFI 600
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Db    541 CPNPKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCILFI 600

Qy    601 ENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACALAASLWLGVLPTLT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACALAASLWLGVLPTLT 660

Qy    661 LGLLVH 666
          ||||||
Db    661 LGLLVH 666


RESULT 2
AAY28552
ID   AAY28552 standard; Peptide; 666 AA.
XX
AC   AAY28552;
XX
DT   19-OCT-1999  (first entry)
XX
DE   SBSEMVL polypeptide #1.
XX
KW   SBSEMVL; semaphorin; axon outgrowth; multidrug resistance; spinal injury;
KW   neurodegeneration; viral infection; cancer.
XX
OS   Homo sapiens.
XX
PN   WO9938885-A2.
XX
PD   05-AUG-1999.
XX
PF   25-JAN-1999;   99WO-EP00422.
XX
PR   30-JAN-1998;   98EP-0300694.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Hayes PD,  Michalovich D;
XX
DR   WPI; 1999-479166/40.
DR   N-PSDB; AAZ00102.
XX
PT   Novel SBSEMVL molecules used for treating neurodegeneration, spinal
PT   injury, neuropathies, and neuromuscular, psychiatric, and
PT   inflammatory disorders, developmental malfunctions, cancer, immune
PT   system disorders and viral infections
XX
PS   Claim 4; Page 29-31; 34pp; English.
XX
CC   This sequence is human SBSEMVL polypeptide #1. SBSEMVL polypeptides are
CC   believed to be members of the Semaphorin family of polypeptides.
CC   Semaphorin polypeptides act as recognition molecules and are involved in
CC   axon outgrowth control. They are also likely to have a role in immune
CC   function and multidrug resistance. SBSEMVL polypeptides may be used for
CC   detecting diseases associated with inappropriate SBSEMVL activity or
CC   levels. SBSEMVL polypeptides and polynucleotides, agonists, antagonists
CC   and antibodies are used to treat neurodegeneration, spinal injury,
CC   neuropathies, and neuromuscular, psychiatric, and inflammatory disorders,
CC   developmental malfunctions, cancer, disorders of the immune system and
CC   viral infection. The polynucleotide is also useful as a source of primers
CC   and probes, and also for detecting the above diseases.
XX
SQ   Sequence   666 AA;

  Query Match            100.0%;  Score 3615;  DB 20;  Length 666;
  Best Local Similarity  100.0%;  Pred. No. 5.3e-304;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MTPPPPGRAAPSAPRARVPGPPARLGLPLRLRLLLLLWAAAASAQGHLRSGPRIFAVWKG 60
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Db      1 MTPPPPGRAAPSAPRARVPGPPARLGLPLRLRLLLLLWAAAASAQGHLRSGPRIFAVWKG 60
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Qy      61 HVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSC 120
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Db      61 HVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSC 120

Qy     121 LDKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVPLGEMRGYAPFSPDENSLV 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LDKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVPLGEMRGYAPFSPDENSLV 180

Qy     181 LFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKI 240
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Db     181 LFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKI 240

Qy     241 YYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKNF 300
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Db     241 YYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKNF 300

Qy     301 NRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFRTSSLKGYHSSLPN 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 NRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFRTSSLKGYHSSLPN 360

Qy     361 PRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQASH 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 PRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQASH 420

Qy     421 GETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVS 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVS 480

Qy     481 SQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSSERSVLQSINPAEPHKE 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 SQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSSERSVLQSINPAEPHKE 540

Qy     541 CPNPKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCILFI 600
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Db     541 CPNPKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCILFI 600

Qy     601 ENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACALAASLWLGVLPTLT 660
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Db     601 ENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACALAASLWLGVLPTLT 660

Qy     661 LGLLVH 666
           ||||||
Db     661 LGLLVH 666
```

ESULT 3
92804
AAW92804 standard; Protein; 666 AA.
XX
AC AAW92804;
XX
DT 07-MAY-1999 (first entry)
XX
DE EP-892047 Seq ID 3.
XX
KW Semaphorin L; human; immunosuppressant; anti-inflammatory; gene therapy;
KW organ transplantation; inflammation therapy; immunotherapy; agonist;
KW immunomodulatory; antagonist.
XX
OS Homo sapiens.
XX
PN EP892047-A2.
XX
PD 20-JAN-1999.
XX
PF 06-JUL-1998; 98EP-0112470.
XX
PR 11-FEB-1998; 98DE-1005371.
PR 09-JUL-1997; 97DE-1029211.
XX
PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
XX
PI Ensser A, Fleckenstein B;

XX
DR WPI; 1999-083564/08.
XX
PT New semaphorin L proteins - used as immunosuppressants and
PT antiinflammatory agents in organ transplants, inflammation therapy,
PT immunotherapy and gene therapy
XX
PS Claim 2; Page 61-64; 135pp; German.
XX
CC This invention describes a novel human semaphorin L protein. This protein
CC or its encoding DNA are useful as immunosuppressants and/or
CC anti-inflammatory agents in organ transplantation, inflammation therapy,
CC immunotherapy and gene therapy. The DNA can be used to produce knock-out
CC or knock-in animals for research purposes. The proteins or DNA can be
CC used to search for the corresponding receptors or to screen for
CC immunomodulatory agonists or antagonists.
XX
SQ Sequence 666 AA;

```
  Query Match             100.0%;  Score 3615;  DB 20;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-304;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MTPPPPGRAAPSAPRARVPGPPARLGLPLRLRLLLLLWAAAASAQGHLRSGPRIFAVWKG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTPPPPGRAAPSAPRARVPGPPARLGLPLRLRLLLLLWAAAASAQGHLRSGPRIFAVWKG 60

Qy      61 HVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 HVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSC 120

Qy     121 LDKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVPLGEMRGYAPFSPDENSLV 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LDKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVPLGEMRGYAPFSPDENSLV 180

Qy     181 LFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKI 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKI 240

Qy     241 YYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKNF 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 YYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKNF 300

Qy     301 NRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFRTSSLKGYHSSLPN 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 NRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFRTSSLKGYHSSLPN 360

Qy     361 PRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQASH 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     421 GETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVS 480
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Qy     481 SQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSSERSVLQSINPAEPHKE 540
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Db     481 SQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSSERSVLQSINPAEPHKE 540

Qy     541 CPNPKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCILFI 600
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Db     541 CPNPKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCILFI 600

Qy     601 ENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACALAASLWLGVLPTLT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACALAASLWLGVLPTLT 660

Qy     661 LGLLVH 666
           ||||||
Db     661 LGLLVH 666
```

RESULT 4

```
AAY82433
ID   AAY82433 standard; Protein; 666 AA.
XX
AC   AAY82433;
XX
DT   27-JUN-2000  (first entry)
XX
DE   Human CDw108 protein SEQ ID NO:1.
XX
KW   Human; CDw108; detection; diagnosis; HIV; infection; anti-HIV.
XX
OS   Homo sapiens.
XX
PN   WO200012700-A1.
XX
PD   09-MAR-2000.
XX
PF   25-AUG-1999;   99WO-JP04571.
XX
PR   26-AUG-1998;   98JP-0239687.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Yamada A,  Kubo K,  Itoh K;
XX
DR   WPI; 2000-246752/21.
DR   N-PSDB; AAA08183.
XX
PT   New CDw108 protein, useful in diagnosis of and as remedy for
PT   CDw108-associated diseases e.g. HIV-1 infection, and in study of
PT   biological functions and molecular specificity of CDw108  -
XX
PS   Claim 1; Fig 1; 73pp; Japanese.
XX
CC   The present sequence represents human CDw108. The CDw109 nucleotide
CC   and protein sequences can be used in the diagnosis and treatment of
CC   CDw108-associated diseases e.g. HIV-1 infection, and in study of
CC   biological functions and molecular specificity of CDw108.
XX
SQ   Sequence   666 AA;

  Query Match            100.0%;  Score 3615;  DB 21;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-304;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MTPPPPGRAAPSAPRARVPGPPARLGLPLRLRLLLLLWAAAASAQGHLRSGPRIFAVWKG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTPPPPGRAAPSAPRARVPGPPARLGLPLRLRLLLLLWAAAASAQGHLRSGPRIFAVWKG 60

Qy      61 HVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 HVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSC 120

Qy     121 LDKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVPLGEMRGYAPFSPDENSLV 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LDKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVPLGEMRGYAPFSPDENSLV 180

Qy     181 LFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKI 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKI 240

Qy     241 YYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKNF 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 YYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKNF 300

Qy     301 NRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFRTSSLKGYHSSLPN 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 NRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFRTSSLKGYHSSLPN 360

Qy     361 PRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQASH 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 PRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQASH 420

Qy     421 GETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVS 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVS 480

Qy     481 SQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSSERSVLQSINPAEPHKE 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 SQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSSERSVLQSINPAEPHKE 540

Qy     541 CPNPKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCILFI 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CPNPKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCILFI 600

Qy     601 ENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACALAASLWLGVLPTLT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACALAASLWLGVLPTLT 660

Qy     661 LGLLVH 666
           ||||||
Db     661 LGLLVH 666


RESULT 5
AAY55009
ID   AAY55009 standard; Protein; 666 AA.
XX
AC   AAY55009;
XX
DT   18-FEB-2000  (first entry)
XX
DE   Human semaphorin, DCSema, protein sequence.
XX
KW   Semaphorin; DCSema; human; inflammatory disease; VESPR; interleukin-12;
KW   IL-12; immune response; aggressive micrometastasising tumour; therapy;
KW   immune suppression; autoimmune disorder; semaphorin receptor;
KW   immune regulation; viral infection.
XX
OS   Homo sapiens.
XX
PN   WO9958676-A2.
XX
PD   18-NOV-1999.
XX
PF   05-MAY-1999;   99WO-US09831.
XX
PR   14-MAY-1998;   98US-0085497.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Spriggs MK;
XX
DR   WPI; 2000-053100/04.
DR   N-PSDB; AAZ40163.
XX
PT   Novel neurological regulator polypeptide for treating inflammatory
PT   diseases, autoimmune disorders, etc.,  -
XX
PS   Claim 1; Page 34-36; 41pp; English.
XX
CC   This sequence is the human semaphorin protein, designated DCSema, of
CC   the invention. DCSema is used for treating inflammatory diseases. DCSema
CC   ligands bind with VESPR to enhance or promote interleukin-12 (IL-12)
CC   production which induces an immune response against aggressive
CC   micrometastasising tumours. They are associated with immune suppression
CC   of mature dendritic cells and therefore can be used for treating
CC   autoimmune disorders. They can be employed to measure biological activity
CC   of any semaphorin receptor in terms of its binding affinity for
CC   semaphorin ligand and also for detecting semaphorin receptor by in vitro
CC   assays. DCSema polypeptides are used as reagents in quality assurance
CC   studies (to monitor shelf life and stability of semaphorin receptor under
CC   different conditions). They are also used as a research tool for studying
CC   the role of this ligand and its receptor in immune regulation and are
CC   also used as carriers for delivering diagnostic or therapeutic agents to
CC   cells expressing semaphorin receptor. They are shown to play a role as
```

```
CC   immune regulators in viral infection.
XX
SQ   Sequence   666 AA;

  Query Match           100.0%;  Score 3615;  DB 21;  Length 666;
  Best Local Similarity  100.0%;  Pred. No. 5.3e-304;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MTPPPPGRAAPSAPRARVPGPPARLGLPLRLRLLLLLWAAAASAQGHLRSGPRIFAVWKG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTPPPPGRAAPSAPRARVPGPPARLGLPLRLRLLLLLWAAAASAQGHLRSGPRIFAVWKG 60

Qy     61 HVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 HVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSC 120

Qy    121 LDKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVPLGEMRGYAPFSPDENSLV 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LDKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVPLGEMRGYAPFSPDENSLV 180

Qy    181 LFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKI 240

Qy    241 YYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKNF 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKNF 300

Qy    301 NRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFRTSSLKGYHSSLPN 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFRTSSLKGYHSSLPN 360

Qy    361 PRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQASH 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQASH 420

Qy    421 GETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVS 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVS 480

Qy    481 SQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSSERSVLQSINPAEPHKE 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 SQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSSERSVLQSINPAEPHKE 540

Qy    541 CPNPKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCILFI 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CPNPKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCILFI 600

Qy    601 ENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACALAASLWLGVLPTLT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACALAASLWLGVLPTLT 660

Qy    661 LGLLVH 666
          ||||||
Db    661 LGLLVH 666


RESULT 6
AAE02650
ID   AAE02650 standard; Protein; 666 AA.
XX
AC   AAE02650;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human Sema7A protein.
XX
KW   Human; Sema7A; semaphorin family; chromosome 15q22.3-q23; stroke;
KW   autoimmune disorder; COPD; chronic obstructive pulmonary disease;
KW   psoriasis; tissue repair; wound healing; irritable bowel syndrome;
KW   inflammation; cancer; atherosclerosis; dendritic cell.
XX
OS   Homo sapiens.
XX
PN   WO200139793-A2.
XX
PD   07-JUN-2001.
XX
PF   28-NOV-2000; 2000WO-EP11873.
XX
PR   30-NOV-1999;   99GB-0028329.
PR   14-SEP-2000; 2000GB-0022572.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Holmes SD,  Lewis CJ;
XX
DR   WPI; 2001-374667/39.
DR   N-PSDB; AAD06126.
XX
PT   Use of Sema7A polypeptides, polynucleotides, or activators or
PT   inhibitors, for manufacturing a medicament for treating autoimmune
PT   disorders, chronic obstructive pulmonary disease, inflammation,
PT   psoriasis and stroke -
XX
PS   Claim 5; Page 28-29; 36pp; English.
XX
CC   The present sequence is human Sema7A protein which
CC   belongs to semaphorin family. The Sema7A gene is located on human
CC   chromosome 15q22.3-q23. The Sema7A polypeptide and polynucleotide
CC   are useful for the manufacture of a medicament for treating autoimmune
CC   disorders, chronic obstructive pulmonary disease (COPD), inflammation,
CC   psoriasis, tissue repair, wounds, to enhance wound healing, irritable
CC   bowel syndrome, stroke, atherosclerosis, cancer or diseases where it is
CC   necessary to promote dendritic cell formation. The polypeptide is also
CC   useful in the diagnostic assays for detecting diseases associated with
CC   inappropriate levels or activities of Sema7A.
XX
SQ   Sequence   666 AA;

  Query Match           100.0%;  Score 3615;  DB 22;  Length 666;
  Best Local Similarity  100.0%;  Pred. No. 5.3e-304;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MTPPPPGRAAPSAPRARVPGPPARLGLPLRLRLLLLLWAAAASAQGHLRSGPRIFAVWKG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTPPPPGRAAPSAPRARVPGPPARLGLPLRLRLLLLLWAAAASAQGHLRSGPRIFAVWKG 60

Qy     61 HVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 HVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSC 120

Qy    121 LDKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVPLGEMRGYAPFSPDENSLV 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LDKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVPLGEMRGYAPFSPDENSLV 180

Qy    181 LFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKI 240

Qy    241 YYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKNF 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKNF 300

Qy    301 NRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFRTSSLKGYHSSLPN 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFRTSSLKGYHSSLPN 360

Qy    361 PRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQASH 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQASH 420

Qy    421 GETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVS 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVS 480
```

```
Qy    481 SQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSSERSVLQSINPAEPHKE 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 SQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSSERSVLQSINPAEPHKE 540

Qy    541 CPNPKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCILFI 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CPNPKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCILFI 600

Qy    601 ENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACALAASLWLGVLPTLT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACALAASLWLGVLPTLT 660

Qy    661 LGLLVH 666
          ||||||
Db    661 LGLLVH 666
```

RESULT 7
AAY56854
ID AAY56854 standard; Protein; 634 AA.
XX
AC AAY56854;
XX
DT 10-APR-2000 (first entry)
XX
DE Human semaphorin K1 polypeptide.
XX
KW Semaphorin K1; cellular physiology; neurite outgrowth; neuron; human;
KW immunogen; pharmaceutical.
XX
OS Homo sapiens.
XX
PN JP11341988-A.
XX
PD 14-DEC-1999.
XX
PF 11-MAR-1999; 99JP-0065672.
XX
PR 11-MAR-1998; 98US-0041236.
XX
PA (EXEL-) EXELIXIS PHARM INC.
XX
DR WPI; 2000-109378/10.
DR N-PSDB; AAZ46841.
XX
PT New semaphorin polypeptides, useful cell physiology modulators and
PT immunogens -
XX
PS Claim 1; Page 12-15; 57pp; Japanese.
XX
CC The invention provided isolated human semaphorin K1 polypeptides. The
CC polypeptides, or nucleic acids encoding them, can be used to modulate
CC cellular physiology by modulating semaphorin K1 activity, e.g. semaphorin
CC K1 polypeptide fragments or antisense nucleic acids can be used to
CC enhance neurite outgrowth from damaged neurons. The polypeptides can also
CC be used as immunogens, reagents for isolating other semaphorins, or as
CC reagents for screening chemical libraries for lead pharmaceutical agents.
CC The nucleic acids can also be used as probes and primers for diagnostic
CC purposes. The present sequence represents the human semaphorin K1
CC polypeptide.
XX
SQ Sequence 634 AA;

```
  Query Match            95.2%;  Score 3443;  DB 21;  Length 634;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-289;
  Matches  634;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     33 LLLLLWAAAASAQGHLRSGPRIFAVWKGHVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGR 92
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 LLLLLWAAAASAQGHLRSGPRIFAVWKGHVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGR 60

Qy     93 GKVYLFDFPEGKNASVRTVNIGSTKGSCLDKRDCENYITLLERRSEGLLACGTNARHPSC 152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GKVYLFDFPEGKNASVRTVNIGSTKGSCLDKRDCENYITLLERRSEGLLACGTNARHPSC 120

Qy    153 WNLVNGTVVPLGEMRGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESEL 212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 WNLVNGTVVPLGEMRGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESEL 180

Qy    213 YTSDTVMQNPQFIKATIVHQDQAYDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGG 272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 YTSDTVMQNPQFIKATIVHQDQAYDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGG 240

Qy    273 ESSLSVSKWNTFLKAMLVCSDAATNKNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYS 332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ESSLSVSKWNTFLKAMLVCSDAATNKNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYS 300

Qy    333 AVCVYSLGDIDKVFRTSSLKGYHSSLPNPRPGKCLPDQQPIPTETFQVADRHPEVAQRVE 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AVCVYSLGDIDKVFRTSSLKGYHSSLPNPRPGKCLPDQQPIPTETFQVADRHPEVAQRVE 360

Qy    393 PMGPLKTPLFHSKYHYQKVAVHRMQASHGETFHVLYLTTDRGTIHKVVEPGEQEHSFAFN 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PMGPLKTPLFHSKYHYQKVAVHRMQASHGETFHVLYLTTDRGTIHKVVEPGEQEHSFAFN 420

Qy    453 IMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCG 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 IMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCG 480

Qy    513 WDQGRCISIYSSERSVLQSINPAEPHKECPNPKPDKAPLQKVSLAPNSRYYLSCPMESRH 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 WDQGRCISIYSSERSVLQSINPAEPHKECPNPKPDKAPLQKVSLAPNSRYYLSCPMESRH 540

Qy    573 ATYSWRHKENVEQSCEPGHQSPNCILFIENLTAQQYGHYFCEAQEGSYFREAQHWQLLPE 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATYSWRHKENVEQSCEPGHQSPNCILFIENLTAQQYGHYFCEAQEGSYFREAQHWQLLPE 600

Qy    633 DGIMAEHLLGHACALAASLWLGVLPTLTLGLLVH 666
          ||||||||||||||||||||||||||||||||||
Db    601 DGIMAEHLLGHACALAASLWLGVLPTLTLGLLVH 634
```

RESULT 8
AAY82434
ID AAY82434 standard; Protein; 664 AA.
XX
AC AAY82434;
XX
DT 27-JUN-2000 (first entry)
XX
DE Mouse CDw108 protein SEQ ID NO:8.
XX
KW Mouse; CDw108; detection; diagnosis; HIV; infection; anti-HIV.
XX
OS Mus musculus.
XX
PN WO200012700-A1.
XX
PD 09-MAR-2000.
XX
PF 25-AUG-1999; 99WO-JP04571.
XX
PR 26-AUG-1998; 98JP-0239687.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
PI Yamada A, Kubo K, Itoh K;
XX
DR WPI; 2000-246752/21.
DR N-PSDB; AAA08189.
XX
PT New CDw108 protein, useful in diagnosis of and as remedy for
PT CDw108-associated diseases e.g. HIV-1 infection, and in study of
PT biological functions and molecular specificity of CDw108 -
XX
PS Example 8; Page 64-69; 73pp; Japanese.

```
XX
CC   The present invention describes human CDw108. The CDw109 nucleotide
CC   and protein sequences can be used in the diagnosis and treatment of
CC   CDw108-associated diseases e.g. HIV-1 infection, and in study of
CC   biological functions and molecular specificity of CDw108. The present
CC   sequence represents mouse CDw108 given in an example from the present
CC   invention.
XX
SQ   Sequence   664 AA;

  Query Match             88.9%;  Score 3214;  DB 21;  Length 664;
  Best Local Similarity   89.1%;  Pred. No. 2.9e-269;
  Matches  594;  Conservative   26;  Mismatches   43;  Indels    4;  Gaps    2;

Qy       1 MTPPPPGRAAPSAPRARVPGPPARLGLPLRLRLLLLLWAAAASAQGHLRSGPRIFAVWKG 60
           ||||||||||||||||||   ||| ||||||||||: | |||||||| |||||| ||||
Db       1 MTPPPPGRAAPSAPRARVLSLPARFGLPLRLRLLLVFWVAAASAQGHSRSGPRISAVWK- 59

Qy      61 HVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSC 120
             ||| ||| | |||||||||||| |||||||||| |:||||||||||||||||||||||
Db      60 --GQDHVDFSQPEPHTVLFHEPGSFSVWVGGRGKVYHFNFPEGKNASVRTVNIGSTKGSC 117

Qy     121 LDKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVV-PLGEMRGYAPFSPDENSL 179
           ||:|| |||||||||  ||| |||||| |||||||| :||  ||||:||||||||||||
Db     118 QDKQDCGNYITLLERRGNGLLVCGTNARKPSCWNLVNDSVVMSLGEMKGYAPFSPDENSL 177

Qy     180 VLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDK 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     178 VLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDK 237

Qy     240 IYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKN 299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db     238 IYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNRN 297

Qy     300 FNRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFRTSSLKGYHSSLP 359
           ||||||||||||||||||||||||||||||||||||||||||:||||||||||   ||
Db     298 FNRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDRVFRTSSLKGYHMGLP 357

Qy     360 NPRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQAS 419
           ||||| ||| :||||||||||| |||||||||||||||||||||||||| |||||||
Db     358 NPRPGMCLPKKQPIPTETFQVADSHPEVAQRVEPMGPLKTPLFHSKYHYQKVVVHRMQAS 417

Qy     420 HGETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYV 479
           :|||||||||||||||||| |:|:||| ||||||||| |||||| :||||:||||||
Db     418 NGETFHVLYLTTDRGTIHKVVESGDQDHSFVFNIMEIQPFHRAAAIQAISLDADRRKLYV 477

       480 SSQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSSERSVLQSINPAEPHK 539
           :||||||||||:|||| |||||||||||||||| ||:|||||:|||||||||||||:
Db     478 TSQWEVSQVPLDMCEVYSGGCHGCLMSRDPYCGWDQDRCVSIYSSQRSVLQSINPAEPHR 537

Qy     540 ECPNPKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCILF 599
           ||||||||:|||||||| |||||:|||||||||| |||:|||||||||||||:||||
Db     538 ECPNPKPDEAPLQKVSLARNSRYYLTCPMESRHATYLWRHEENVEQSCEPGHQSPSCILF 597

Qy     600 IENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACALAASLWLGVLPTL 659
           ||||||:||||| |||||||| ||||||:||||| :|| |:||| ||||| ||||||||
Db     598 IENLTARQYGHYRCEAQEGSYLREAQHWELLPEDRALAEQLMGHARALAASFWLGVLPTL 657

Qy     660 TLGLLVH 666
           |||||||
Db     658 ILGLLVH 664


RESULT 9
AAB93440
ID   AAB93440 standard; Protein; 379 AA.
XX
AC   AAB93440;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human protein sequence SEQ ID NO:12678.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 12678; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence   379 AA;

  Query Match             57.5%;  Score 2079;  DB 22;  Length 379;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-171;
  Matches  379;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     288 MLVCSDAATNKNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFR 347
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLVCSDAATNKNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFR 60

Qy     348 TSSLKGYHSSLPNPRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLFHSKYH 407
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TSSLKGYHSSLPNPRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLFHSKYH 120

Qy     408 YQKVAVHRMQASHGETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQT 467
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 YQKVAVHRMQASHGETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQT 180

Qy     468 MSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSSERS 527
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    181 MSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSSERS 240

Qy    528 VLQSINPAEPHKECPNPKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSC 587
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 VLQSINPAEPHKECPNPKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSC 300

Qy    588 EPGHQSPNCILFIENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACAL 647
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 EPGHQSPNCILFIENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACAL 360

Qy    648 AASLWLGVLPTLTLGLLVH 666
          |||||||||||||||||||
Db    361 AASLWLGVLPTLTLGLLVH 379


RESULT 10
AAW92805
ID   AAW92805 standard; Protein; 394 AA.
XX
AC   AAW92805;
XX
DT   07-MAY-1999  (first entry)
XX
DE   EP-892047 Seq ID 4.
XX
KW   Semaphorin L; human; immunosuppressant; anti-inflammatory; gene therapy;
KW   organ transplantation; inflammation therapy; immunotherapy; agonist;
KW   immunomodulatory; antagonist.
XX
OS   Homo sapiens.
XX
PN   EP892047-A2.
XX
PD   20-JAN-1999.
XX
PF   06-JUL-1998;   98EP-0112470.
XX
PR   11-FEB-1998;   98DE-1005371.
PR   09-JUL-1997;   97DE-1029211.
XX
PA   (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.
XX
PI   Ensser A,  Fleckenstein B;
XX
DR   WPI; 1999-083564/08.
XX
PT   New semaphorin L proteins - used as immunosuppressants and
PT   antiinflammatory agents in organ transplants, inflammation therapy,
PT   immunotherapy and gene therapy
XX
PS   Claim 4; Page 64-65; 135pp; German.
XX
CC   This invention describes a novel human semaphorin L protein. This protein
CC   or its encoding DNA are useful as immunosuppressants and/or
CC   anti-inflammatory agents in organ transplantation, inflammation therapy,
CC   immunotherapy and gene therapy. The DNA can be used to produce knock-out
CC   or knock-in animals for research purposes. The proteins or DNA can be
CC   used to search for the corresponding receptors or to screen for
CC   immunomodulatory agonists or antagonists.
XX
SQ   Sequence   394 AA;

  Query Match           52.5%;  Score 1897;  DB 20;  Length 394;
  Best Local Similarity  90.2%;  Pred. No. 1.6e-155;
  Matches  358;  Conservative    8;  Mismatches   27;  Indels    4;  Gaps    2;

Qy      1 MTPPPPGRAAPSAPRARVPGPPARLGLPLRLRLLLLLWAAAASAQGHLRSGPRIFAVWKG 60
          ||||||||||||||||||   ||| ||||||||||: | ||||||| |||||| ||||
Db      1 MTPPPPGRAAPSAPRARVLSLPARFGLPLRLRLLLVFWVAAASAQGHSRSGPRISAVWK- 59

Qy     61 HVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSC 120
             ||| ||| | |||||||||||| |||||||||| |:|||||||||||||||||||||
Db     60 --GQDHVDFSQPEPHTVLFHEPGSFSVWVGGRGKVYHFNFPEGKNASVRTVNIGSTKGSC 117

Qy    121 LDKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVV-PLGEMRGYAPFSPDENSL 179
            ||:|| |||||||||  ||| |||||| |||||||| :||  ||||:||||||||||||
Db    118 QDKQDCGNYITLLERRGNGLLVCGTNARKPSCWNLVNDSVVMSLGEMKGYAPFSPDENSL 177

Qy    180 VLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDK 239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    178 VLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDK 237

Qy    240 IYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKN 299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db    238 IYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNRN 297

Qy    300 FNRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDKVFRTSSLKGYHSSLP 359
          ||||||||||||||||||||||||||||||||||||||:||||||||||| |
Db    298 FNRLQDVFLLPDPSGQWRDTRVYGVFSNPWNYSAVCVYSLGDIDRVFRTSSLKGYHMGLS 357

Qy    360 NPRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGP 396
          ||||| ||| :|||||||||||| ||||||||||||
Db    358 NPRPGMCLPKKQPIPTETFQVADSHPEVAQRVEPMGP 394


RESULT 11
AAY56855
ID   AAY56855 standard; Protein; 606 AA.
XX
AC   AAY56855;
XX
DT   10-APR-2000  (first entry)
XX
DE   Semaphorin K1 polypeptide related sequence.
XX
KW   Semaphorin K1; cellular physiology; neurite outgrowth; neuron; human;
KW   immunogen; pharmaceutical.
XX
OS   Unidentified.
XX
PN   JP11341988-A.
XX
PD   14-DEC-1999.
XX
PF   11-MAR-1999;   99JP-0065672.
XX
PR   11-MAR-1998;   98US-0041236.
XX
PA   (EXEL-) EXELIXIS PHARM INC.
XX
DR   WPI; 2000-109378/10.
DR   N-PSDB; AAZ46842.
XX
PT   New semaphorin polypeptides, useful cell physiology modulators and
PT   immunogens -
XX
PS   Disclosure; Page 17-20; 57pp; Japanese.
XX
CC   The invention provided isolated human semaphorin K1 polypeptides. The
CC   polypeptides, or nucleic acids encoding them, can be used to modulate
CC   cellular physiology by modulating semaphorin K1 activity, e.g. semaphorin
CC   K1 polypeptide fragments or antisense nucleic acids can be used to
CC   enhance neurite outgrowth from damaged neurons. The polypeptides can also
CC   be used as immunogens, reagents for isolating other semaphorins, or as
CC   reagents for screening chemical libraries for lead pharmaceutical agents.
CC   The nucleic acids can also be used as probes and primers for diagnostic
CC   purposes.
XX
SQ   Sequence   606 AA;

  Query Match           37.2%;  Score 1345.5;  DB 21;  Length 606;
  Best Local Similarity  45.9%;  Pred. No. 1.9e-107;
  Matches  274;  Conservative   85;  Mismatches  227;  Indels   11;  Gaps    6;

Qy     27 LPLRLRLLLLLWAAAASAQGHLRSGPRIFAVWKGHVGQDRVDFGQTEPHTVLFHEPGSSS 86
          | : :|||::| :|  :|:      ||:    .  || |  ||  |||||||   ||
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Db       4 LCVSIRLLMIL-SAITAAKSRFIDKPRLIVNLTDGFGQHRF-FGPQEPHTVLFHSLNSSD 61

Qy      87 VWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSCLDKRDCENYITLLERRSEGLLACGTN 146

Db      62 VYVGGNNTIYLFDFAHSSNASTALINITSTHNTHRLSSTCENFITLLHNQTDGLLACGTN 121

Qy     147 ARHPSCWNLVNGTVVPLGEMRGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRI 206

Db     122 SQKPSCWLINNLTTQFLGPKLGLAPFSPSSGNLVLFDQNDTYSTINLYKSLSGSHKFRRI 181

Qy     207 RGESELYTSDTVMQNPQFIKATIVHQDQAYDDKIYYFFREDNPDKNPEAPLNVSRVAQLC 266

Db     182 AGQVELYTSDTAMHRPQFVQATAVHKNESYDDKIYFFFQENSHSDFKQFPHTVPRVGQVC 241

Qy     267 RGDQGGESSLSVSKWNTFLKAMLVCSDAATNKNFNRLQDVFLLPDPSGQWRDTRVYGVFS 326

Db     242 SSDQGGESSLSVYKWTTFLKARLACVDYDTGRIYNELQDIFIWQAPENSWEETLIYGLFL 301

       327 NPWNYSAVCVYSLGDIDKVFRTSSLKGYHSSLPNPRPGKCLPDQQPIPTETFQVADRHPE 386

Db     302 SPWNFSAVCVFTVKDIDHVFKTSKLKNYHHKLPTPRPGQCMKNHQHVPTETFQVADRYPE 361

Qy     387 VAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQASHGETF--HVLYLTTDRGTIHKVVEPGE 444

Db     362 VADPVYQKNNAMFPIIQSKYIYTKLLVYRVE--YGGVFWATIFYLTTIKGTIHIYVRYED 419

Qy     445 QEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHGCL 504

Db     420 SNSTTALNILEINPFQKPAPIQNILLDNTNLKLYVNSEWEVSEVPLDLCSVYGNDCFSCF 479

Qy     505 MSRDPYCGWDQGRCISIYSSERSVLQSINPAEP--HKECPNPKPDKAPLQKVSLAPNSRY 562

Db     480 MSRDPLCTWYNNTC---SFKQRVSVETGGPANRTLSEMCGDHYAPTVVKHQVSIPLLSNS 536

Qy     563 YLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCILFIENLTAQQYGHYFCEAQEGS 619

Db     537 YLSCPAVSNHADYFWTKDGFTEKRCHVKTHKNDCILLIANSTTATNGTHVCNMKEDS 593


RESULT 12
AAY28553
ID   AAY28553 standard; Peptide; 215 AA.
XX
AC   AAY28553;
XX
     19-OCT-1999  (first entry)

     SBSEMVL polypeptide #2.
XX
KW   SBSEMVL; semaphorin; axon outgrowth; multidrug resistance; spinal injury;
KW   neurodegeneration; viral infection; cancer.
XX
OS   Homo sapiens.
XX
PN   WO9938885-A2.
XX
PD   05-AUG-1999.
XX
PF   25-JAN-1999;   99WO-EP00422.
XX
PR   30-JAN-1998;   98EP-0300694.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Hayes PD,  Michalovich D;
XX
DR   WPI; 1999-479166/40.
DR   N-PSDB; AAZ00103.
XX
PT   Novel SBSEMVL molecules used for treating neurodegeneration, spinal
PT   injury, neuropathies, and neuromuscular, psychiatric, and
PT   inflammatory disorders, developmental malfunctions, cancer, immune
PT   system disorders and viral infections
XX
PS   Claim 17; Page 32; 34pp; English.
XX
CC   This sequence is human SBSEMVL polypeptide #2. SBSEMVL polypeptides are
CC   believed to be members of the Semaphorin family of polypeptides.
CC   Semaphorin polypeptides act as recognition molecules and are involved in
CC   axon outgrowth control. They are also likely to have a role in immune
CC   function and multidrug resistance. SBSEMVL polypeptides may be used for
CC   detecting diseases associated with inappropriate SBSEMVL activity or
CC   levels. SBSEMVL polypeptides and polynucleotides, agonists, antagonists
CC   and antibodies are used to treat neurodegeneration, spinal injury,
CC   neuropathies, and neuromuscular, psychiatric, and inflammatory disorders,
CC   developmental malfunctions, cancer, disorders of the immune system and
CC   viral infection. The polynucleotide is also useful as a source of primers
CC   and probes, and also for detecting the above diseases.
XX
SQ   Sequence  215 AA;

  Query Match             28.5%;  Score 1029;  DB 20;  Length 215;
  Best Local Similarity   91.6%;  Pred. No. 1e-80;
  Matches  197;  Conservative    2;  Mismatches   14;  Indels    2;  Gaps    2;

Qy      63 GQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSCLD 122

Db       1 GQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTKGSCLD 60

Qy     123 KRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVPLGEMRGYAPFSPDEN-SLVL 181

Db      61 KRDCENYITLLERRSEGLLACGTNARHPSCWNLVNALWCHLGESGGYAPFSPDENVPWFC 120

Qy     182 FEGDEVYSTIRK-QEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKI 240

Db     121 FEGDEVYSTIRKARNYNWEDPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKI 180

Qy     241 YYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESS 275

Db     181 YYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESS 215


RESULT 13
ABB97964
ID   ABB97964 standard; Protein; 893 AA.
XX
AC   ABB97964;
XX
DT   06-SEP-2002  (first entry)
XX
DE   Human protein sequence #31.
XX
KW   Human; brain; tonsil; hippocampus; foetal brain; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO200252005-A1.
XX
PD   04-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-JP11217.
XX
PR   22-DEC-2000; 2000JP-0389742.
XX
PA   (KAZU-) KAZUSA DNA RES INST FOUND.
PA   (CELE-) CELESTAR LEXICO-SCI LTD.
XX
PI   Ohara O,  Nagase T,  Nakajima D;
XX
DR   WPI; 2002-500762/53.
DR   N-PSDB; ABN83984.
XX
PT   Genes and their expression products cloned from human cDNA libraries
PT   for treatment and diagnosis of diseases associated with their
PT   expression -
XX
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PS   Claim 1(a); Page 126-132; 238pp; Japanese.
XX
CC   The invention relates to DNA encoding polypeptides directly cloned from
CC   cDNA libraries originating in adult whole brain, human tonsil, human
CC   adult hippocampus and human foetal whole brain. Polypeptides and
CC   polynucleotides of the invention may be used in the investigation of
CC   differential expression of the DNA sequences in normal subjects and
CC   disease patients. They may also be used in the production of antibodies,
CC   oligonucleotide probes and DNA chips for diagnosis and identification
CC   of drugs for treatment of diseases with which the DNA sequences are
CC   associated. The sequences given in records ABB97934-ABB97964 represent
CC   human proteins of the invention.
XX
SQ   Sequence   893 AA;

  Query Match             18.8%;  Score 680.5;  DB 23;  Length 893;
  Best Local Similarity   30.1%;  Pred. No. 1.5e-49;
  Matches  220;  Conservative   89;  Mismatches  293;  Indels  129;  Gaps   29;

Qy       4 PPPGRAAPSAPRARVPGPPA------RLGL---------------PLRLRLLLLL----- 37
Db      35 PPVSPAEPPEPEPRDTVAPALRMLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLQPP 94

Qy      38 ---WAAAASAQGHLRSGPRIFAVWKGHVGQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGK 94
Db      95 PPTWALSPRISLPLGSEERPFL---------RFEAEHISNYTALLLSRDGRTLYVGAREA 145

Qy      95 VY-----LFDFPEGKNASVRTVNIGSTKGSCLDK-----RDCENYI-TLLERRSEGLLAC 143
Db     146 LFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKGKDPQRDCQNYIKILLPLSGSHLFTC 205

Qy     144 GTNARHPSCW--NLVNGTV-------VPLGEMRGYAPFSPDENSLVLFEGDEVYSTIRKQ 194
Db     206 GTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCPFDPNFKSTALVVDGELY-TGTVS 264

Qy     195 EYNGKIPRFRRIRGESELYTSDTV--MQNPQFIKATIVHQD----QAYDDKIYYFFREDN 248
Db     265 SFQGNDPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPESLGSLQGDDDKIYFFFSETG 324

Qy     249 PDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKNFNRLQDVFL 308
Db     325 QEFEFFENTIVSRIARICKGDEGGERVLQ-QRWTSFLKAQLLCSRPDDGFPFNVLQDVFT 383

Qy     309 LPDPSGQWRDTRVYGVFSNPWNY-----SAVCVYSLGDIDKVF---------RTSSLKGY 354
Db     384 LSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSGLYKEVNRETQQWYTV 443

Qy     355 HSSLPNPRPGKCLPD--QQPIPTETFQVADR----------HPEVAQRVEPMGPLKTPL 401
Db     444 THPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVRSRMLLLQP----- 498

       402 FHSKYHYQKVAVHRMQASHGETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRR 461
Db     499 ---QARYQRVAVHRVPGLH-HTYDVLFLGTGDGRLHKAVSVGPRVHI----IEELQIFSS 550

Qy     462 AAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRC--I 519
Db     551 GQPVQNLLLDTHRGLLYAASHSGVVQVPMANCSLY-RSCGDCLLARDPYCAWSGSSCKHV 609

Qy     520 SIYSSE---RSVLQSINPAEPHKEC-------PNPKP-DKAPLQKVSLAPNSRYYLSCPM 568
Db     610 SLYQPQLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCEQVQFQPNTVNTLACPL 669

Qy     569 ESRHATYSWRHK---ENVEQSCEPGHQSPNCILFIENLTAQQYGHYFC-EAQEGSYFREA 624
Db     670 LSNLATRLWLRNGAPVNASASC---HVLPTGDLLL--VGTQQLGEFQCWSLEEGFQQLVA 724

Qy     625 QHWQLLPEDGI 635
Db     725 SYCPEVVEDGV 735


RESULT 14
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AAE03818
ID   AAE03818 standard; Protein; 832 AA.
XX
AC   AAE03818;
XX
DT   08-AUG-2001  (first entry)
XX
DE   Human gene 1 encoded secreted protein HKAHL26, SEQ ID NO: 64.
XX
KW   Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KW   foetal abnormality; developmental abnormality; haematopoietic disorder;
KW   immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW   Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW   psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW   inflammation; neurological disorder; Alzheimer's disease; food additive;
KW   angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy;
KW   pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW   cell culture; chemotaxis; vulnerary; binding partner identification;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1..38
FT                    /label= Signal_peptide
FT   Protein          39..832
FT                    /note= "Mature secreted protein"
XX
PN   WO200136440-A1.
XX
PD   25-MAY-2001.
XX
PF   15-NOV-2000; 2000WO-US31282.
XX
PR   19-NOV-1999;   99US-0166414.
PR   21-JUL-2000; 2000US-0219665.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Komatsoulis GA,  Birse CE,  Moore PA;
XX
DR   WPI; 2001-343795/36.
DR   N-PSDB; AAD08283.
XX
PT   Isolated nucleic acid molecule encoding a human secreted protein is
PT   used in preventing, treating or ameliorating a medical condition  -
XX
PS   Claim 11; Page 476-479; 553pp; English.
XX
CC   AAD08283-AAD08355 represent cDNAs corresponding to 23 human secreted
CC   protein genes, and AAE03818-AAE03870 represent the proteins they encode.
CC   AAE03871-AAE03896 represent human secreted protein fragments or variants.
CC   The secreted proteins and their genes are useful for preventing,
CC   treating or ameliorating medical conditions, e.g., by protein or gene
CC   therapy. Pathological conditions can be diagnosed by determining the
CC   amount of the new protein in a sample or by determining the presence of
CC   mutations in the new genes. Specific uses are described for each of the
CC   23 genes, based on the tissues in which they are most highly expressed,
CC   and include developing products for the diagnosis or treatment of
CC   proliferative disorders, cancer, tumours, foetal and developmental
CC   abnormalities, haematopoietic disorders, diseases of the immune system,
CC   AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC   allergies, neurological disorders (e.g., Alzheimer's disease,
CC   Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC   skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC   cardiovascular disorders, angiogenic disorders, kidney disorders,
CC   gastrointestinal disorders, pregnancy-related disorders, endocrine
CC   disorders, and infections. The proteins can also be used to aid wound
CC   healing and epithelial cell proliferation, to prevent skin aging due to
CC   sunburn, to maintain organs before transplantation, for supporting cell
CC   culture of primary tissues, to regenerate tissues, to identify their
CC   cognate ligands or binding partners, and in chemotaxis, and can be used
CC   as a food additive or preservative to modify storage properties.
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CC   Antibodies specific for a protein of the invention can be used in
CC   alleviating symptoms associated with the disorders mentioned above, and
CC   in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC   immunosorbent assay (ELISA). The present sequence represents a human
CC   secreted protein of the invention.
XX
SQ   Sequence   832 AA;

 Query Match             18.7%;  Score 674.5;  DB 22;  Length 832;
 Best Local Similarity   30.5%;  Pred. No. 4.4e-49;
 Matches  214;  Conservative   90;  Mismatches  285;  Indels  113;  Gaps   28;

Qy      12 SAPRARVPGPPARLGLPLRLRLLLLL--------WAAAASAQGHLRSGPRIFAVWKGHVG 63
Db       8 AAPWGALPPRP-----PLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFL------- 55

Qy      64 QDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVY-----LFDFPEGKNASVRTVNIGSTKG 118
Db      56 --RFEAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQ 113

Qy     119 SCLDK-----RDCENYI-TLLERRSEGLLACGTNARHPSCW--NLVNGTV-------VPL 163
Db     114 QCSFKGKDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLL 173

Qy     164 GEMRGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTV--MQN 221
Db     174 EDGKGRCPFDPNFKSTALVVDGELY-TGTVSSFQGNDPAISRSQSLRPTKTESSLNWLQD 232

Qy     222 PQFIKATIVHQD----QAYDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLS 277
Db     233 PAFVASAYIPESLGSLQGDDDKIYFFFSETGQEFEFFENTIVSRIARICKGDEGGERVLQ 292

Qy     278 VSKWNTFLKAMLVCSDAATNKNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPWNY-----S 332
Db     293 -QRWTSFLKAQLLCSRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGS 351

Qy     333 AVCVYSLGDIDKVF---------RTSSLKGYHSSLPNPRPGKCLPD--QQPIPTETFQVA 381
Db     352 AVCVFTMKDVQRVFSGLYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLP 411

Qy     382 DR-----------HPEVAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQASHGETFHVLYLT 430
Db     412 DRVLNFLKDHFLMDGQVRSRMLLLQP--------QARYQRVAVHRVPGLH-HTYDVLFLG 462

Qy     431 TDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPL 490
Db     463 TGDGRLHKAVSVGPRVHI----IEELQIFSSGQPVQNLLLDTHRGLLYAASHSGVVQVPM 518

Qy     491 DLCEVYGGGCHGCLMSRDPYCGWDQGRC--ISIYSSE---RSVLQSINPAEPHKEC---- 541
Db     519 ANCSLY-RSCGDCLLARDPYCAWSGSSCKHVSLYQPQLATRPWIQDIEGASAKDLCSASS 577

Qy     542 ---PNPKP-DKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHK---ENVEQSCEPGHQSP 594
Db     578 VVSPSFVPTGEKPCEQVQFQPNTVNTLACPLLSNLATRLWLRNGAPVNASASC---HVLP 634

Qy     595 NCILFIENLTAQQYGHYFC-EAQEGSYFREAQHWQLLPEDGI 635
Db     635 TGDLLL--VGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGV 674


RESULT 15
ABG64522
ID   ABG64522 standard; Protein; 832 AA.
XX
AC   ABG64522;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Human albumin fusion protein #1197.
XX
KW   Albumin fusion protein; therapeutic protein X; human albumin; HA;
KW   human serum albumin; HSA; cancer; reproductive disorder;
KW   digestive disorder; immune disorder; endocrine disorder;
KW   haematopoietic disorder; neural disorder; connective disorder;
KW   cytostatic; antiinfertility; antiinflammatory; antiulcer;
KW   immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
KW   neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
KW   osteopathic; antiarthritic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200177137-A1.
XX
PD   18-OCT-2001.
XX
PF   12-APR-2001; 2001WO-US11988.
XX
PR   12-APR-2000; 2000US-229358P.
PR   25-APR-2000; 2000US-199384P.
PR   21-DEC-2000; 2000US-256931P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Haseltine WA;
XX
DR   WPI; 2002-010886/01.
XX
PT   New fusion protein for treating disease e.g. diabetes comprises an
PT   albumin fused to a therapeutic protein -
XX
PS   Claim 1; Page 1288-1291; 2102pp; English.
XX
CC   The present invention relates to albumin fusion proteins comprising a
CC   therapeutic protein X and human albumin (HA, also known as human serum
CC   albumin, HSA). The proteins are useful for treating a disease or
CC   disorder that may be modulated by therapeutic protein X. The albumin
CC   extends the shelf-life of protein X, and may increase its biological
CC   in vitro/in vivo activity. The protein is useful for treating and
CC   diagnosing disorders such as cancer, reproductive disorders, digestive
CC   disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders
CC   (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders
CC   (e.g. diabetes), haematopoietic disorders, neural disorders
CC   (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,
CC   encephalomyelitis, meningitis, schizophrenia), and connective disorders
CC   (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin
CC   fusion proteins of the invention.
XX
SQ   Sequence   832 AA;

 Query Match             18.7%;  Score 674.5;  DB 23;  Length 832;
 Best Local Similarity   30.5%;  Pred. No. 4.4e-49;
 Matches  214;  Conservative   90;  Mismatches  285;  Indels  113;  Gaps   28;

Qy      12 SAPRARVPGPPARLGLPLRLRLLLLL--------WAAAASAQGHLRSGPRIFAVWKGHVG 63
Db       8 AAPWGALPPRP-----PLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFL------- 55

Qy      64 QDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVY-----LFDFPEGKNASVRTVNIGSTKG 118
Db      56 --RFEAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQ 113

Qy     119 SCLDK-----RDCENYI-TLLERRSEGLLACGTNARHPSCW--NLVNGTV-------VPL 163
Db     114 QCSFKGKDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLL 173

Qy     164 GEMRGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTV--MQN 221
Db     174 EDGKGRCPFDPNFKSTALVVDGELY-TGTVSSFQGNDPAISRSQSLRPTKTESSLNWLQD 232

Qy     222 PQFIKATIVHQD----QAYDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLS 277
Db     233 PAFVASAYIPESLGSLQGDDDKIYFFFSETGQEFEFFENTIVSRIARICKGDEGGERVLQ 292

Qy     278 VSKWNTFLKAMLVCSDAATNKNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPWNY-----S 332
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          :| :|||| |:||       || ||||| |      ||||  |||||:: |:      |
Db    293 -QRWTSFLKAQLLCSRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGS 351

Qy    333 AVCVYSLGDIDKVF---------RTSSLKGYHSSLPNPRPGKCLPD--QQPIPTETFQVA 381
          ||||::: |: :||          |         :| |||| |: :  ::     : |:
Db    352 AVCVFTMKDVQRVFSGLYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLP 411

Qy    382 DR-----------HPEVAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQASHGETFHVLYLT 430
          ||             :|  |:  : |        :  ||:|||||:   |  |: ||:|
Db    412 DRVLNFLKDHFLMDGQVRSRMLLLQP--------QARYQRVAVHRVPGLH-HTYDVLFLG 462

Qy    431 TDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPL 490
          |  | :|| |  | : |     | |:| |     :| : ||  |  || :|   | |||:
Db    463 TGDGRLHKAVSVGPRVHI----IEELQIFSSGQPVQNLLLDTHRGLLYAASHSGVVQVPM 518

Qy    491 DLCEVYGGGCHGCLMSRDPYCGWDQGRC--ISIYSSE---RSVLQSINPAEPHKEC---- 541
            | :|   |  ||::|||| |    |  :|:|  :   |  :| |  |     |
Db    519 ANCSLY-RSCGDCLLARDPYCAWSGSSCKHVSLYQPQLATRPWIQDIEGASAKDLCSASS 577

Qy    542 ---PNPKP-DKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHK---ENVEQSCEPGHQSP 594
            |:  |  : | ::|   ||:   |:||: |  ||  |       |   ||   |  |
Db    578 VVSPSFVPTGEKPCEQVQFQPNTVNTLACPLLSNLATRLWLRNGAPVNASASC---HVLP 634

      595 NCILFIENLTAQQYGHYFC-EAQEGSYFREAQHWQLLPEDGI 635
          | :  :  || | : |   :||     | :   : |||:
Db    635 TGDLLL--VGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGV 674

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